

WHAT IS CLAIMED IS:

1. An isolated nucleic acid fragment comprising a sequence of at least about 10 nucleotides from a *Brassicaceae* or *Helianthus* delta-12 fatty acid desaturase gene having at least one mutation, wherein said gene is effective for altering fatty acid composition in *Brassicaceae* or *Helianthus* seeds and wherein said sequence includes said at least one mutation.
2. The nucleic acid fragment of claim 1, wherein said at least one mutation comprises a mutation in a region of said desaturase gene encoding a His-Glu-Cys-Gly-His amino acid motif.
3. The nucleic acid fragment of claim 2, wherein said at least one mutation comprises a non-conservative amino acid substitution in said region.
4. An isolated nucleic acid fragment comprising a sequence of at least about 10 nucleotides from a *Brassicaceae* or *Helianthus* delta-15 fatty acid desaturase gene having at least one mutation, wherein said gene is effective for altering fatty acid composition in *Brassicaceae* or *Helianthus* seeds and wherein said sequence includes said at least one mutation.
5. The nucleic acid fragment of claim 4, wherein said at least one mutation comprises a mutation in a region of said desaturase gene encoding a His-Asp-Cys-Gly-His amino acid motif.

6. The nucleic acid fragment of claim 5, wherein said at least one mutation comprises a non-conservative amino acid substitution in said region.

7. An isolated nucleic acid fragment encoding a polypeptide having an amino acid sequence selected from the group consisting of: an amino acid sequence substantially identical to SEQ ID NO:12, an amino acid sequence substantially identical to SEQ ID NO:16 and an amino acid sequence substantially identical to SEQ ID NO:18.

8. The nucleic acid fragment of claim 7, wherein said amino acid sequence is SEQ ID NO:12.

9. The nucleic acid fragment of claim 7, wherein said amino acid sequence is SEQ ID NO:16.

10. The nucleic acid fragment of claim 7, wherein said amino acid sequence is SEQ ID NO:18.

11. An isolated nucleic acid fragment, wherein said nucleic acid fragment is selected from the group consisting of:

- a) SEQ ID NO:11;
- b) SEQ ID NO:15;
- c) SEQ ID NO:17;
- d) an RNA analog of SEQ ID NO:11;
- e) an RNA analog of SEQ ID NO:15;
- f) an RNA analog of SEQ ID NO:17;
- g) a nucleic acid fragment having a nucleic acid sequence complementary to a), b), c), d), e), or f); and
- h) a nucleic acid fragment of a), b), c), d), e), f), or g), that is at least 10 nucleotides in length and

that hybridizes under stringent conditions to genomic DNA encoding the mutation in the polypeptide of SEQ ID NO:12, SEQ ID NO:16, or SEQ ID NO:18.

12. An isolated polypeptide having an amino acid  
5 sequence selected from the group consisting of: an amino acid sequence substantially identical to SEQ ID NO:12, an amino acid sequence substantially identical to SEQ ID NO:16, and an amino acid sequence substantially identical to SEQ ID NO:18.
- 10 13. The polypeptide of claim 12, wherein said amino acid sequence is SEQ ID NO:12.
14. The polypeptide of claim 12, wherein said amino acid sequence is SEQ ID NO:16.
- 15 15. The polypeptide of claim 12, wherein said amino acid sequence is SEQ ID NO:18.
16. A *Brassicaceae* or *Helianthus* plant, said plant containing first and second delta-12 fatty acid desaturase genes, each said gene having at least one mutation, wherein at least one of said mutations is in a region encoding a  
20 His-Xaa-Xaa-Xaa-His amino acid motif and wherein each said mutation confers an altered fatty acid composition in seeds of said plant.
17. The plant of claim 16, wherein said motif comprises the sequence His-Glu-Cys-Gly-His.

18. The plant of claim 17, wherein said mutation comprises a non-conservative amino acid substitution in said region.

19. The plant of claim 16, wherein said fatty acid composition comprises, following crushing and extraction of said seeds, from about 1% to about 10% linoleic acid based on total fatty acid composition.

20. A *Brassicaceae* or *Helianthus* plant containing a sequence of at least 10 nucleotides from a delta-15 fatty acid desaturase gene having at least one mutation, said at least one mutation in a region encoding a His-Xaa-Xaa-Xaa-His amino acid motif and wherein said mutation confers an altered fatty acid composition in seeds of said plant.

21. The plant of claim 20, wherein said motif comprises the sequence His-Asp-Cys-Gly-His.

22. The plant of claim 21, wherein said mutation comprises a non-conservative amino acid substitution in said region.

23. The plant of claim 20, wherein said fatty acid composition comprises, following crushing and extraction of said seeds, from about 0.5% to about 10%  $\alpha$ -linolenic acid based on total fatty acid composition.

24. A *Brassicaceae* or *Helianthus* plant containing:

a) a sequence of at least about 10 nucleotides from a delta-12 fatty acid desaturase gene having at least one mutation, said at least one delta-12 gene mutation in a region encoding a His-Xaa-Xaa-Xaa-His amino acid motif; and

b) a sequence of at least about 10 nucleotides from a delta-15 fatty acid desaturase gene having at least one mutation, said at least one delta-15 gene mutation in a region encoding a His-Xaa-Xaa-Xaa-His amino acid motif, said  
5 delta-12 gene mutation and said delta-15 gene mutation conferring an altered fatty acid composition in seeds of said plant.

25. A *Brassicaceae* or *Helianthus* plant containing a sequence of at least about 10 nucleotides from a delta-12  
10 fatty acid desaturase gene having at least one mutation, said at least one mutation in a region encoding a Tyr-Leu-Asn-Asn-Pro amino acid motif and wherein said mutation confers an altered fatty acid composition in seeds of said plant.

15 26. A method for producing a *Brassicaceae* or *Helianthus* plant line, comprising the steps of:

a) inducing mutagenesis in cells of a starting variety of a *Brassicaceae* or *Helianthus* species;

20 b) obtaining one or more progeny plants from said cells;

c) identifying at least one of said progeny plant that contains a delta-12 fatty acid desaturase gene having at least one mutation, said at least one mutation in a region encoding a His-Xaa-Xaa-Xaa-His amino acid motif; and

25 d) producing said plant line from said at least one progeny plant by self- or cross-pollination, said plant line having said at least one delta-12 gene mutation.

27. The method of claim 26, wherein said plant line produces seeds yielding an oil having a linoleic acid  
30 content from about 1% to about 14%.

28. The method of claim 26, further comprising the steps of:

e) inducing mutagenesis in cells of said plant line;

5 f) obtaining one or more progeny plants from said plant line cells;

g) identifying at least one of said plant line progeny plants that contains a delta-15 fatty acid desaturase gene having at least one delta-15 gene mutation, said at least one delta-15 gene mutation in a region  
10 encoding a His-Xaa-Xaa-Xaa-His amino acid motif;

h) producing a second plant line from said at least one plant line progeny plant by self- or cross-pollination, said second plant line having said at least one delta-12 gene mutation and said at least one delta-15 gene mutation.

15 29. The method of claim 26, wherein said starting variety is a *Brassica napus* variety.

30. A method for producing a *Brassicaceae* plant line, comprising the steps of:

20 a) inducing mutagenesis in cells of a starting variety of a *Brassicaceae* species;

b) obtaining one or more progeny plants from said cells;

25 c) identifying at least one of said progeny plants that contains a delta-12 fatty acid desaturase gene having at least one mutation, said at least one mutation in a region encoding a His-Xaa-Xaa-Xaa-His amino acid motif;

d) producing a first plant line from said at least one progeny plant by self- or cross-pollination, said plant line having said at least one delta-12 gene mutation;

30 e) inducing mutagenesis in cells of said first plant line;

f) obtaining one or more progeny plants from said first plant line cells;

g) identifying at least one of said first plant line progeny plants that contains a second delta-12 fatty acid desaturase gene having at least one mutation, said second gene mutation in a region other than a region encoding a His-Xaa-Xaa-Xaa-His amino acid motif; and

h) producing a second plant line from said at least one plant line progeny plant by self- or cross-pollination, said second plant line having said first delta-12 gene mutation and said second delta-12 gene mutation.

31. A method for producing a *Brassicaceae* or *Helianthus* plant line, comprising the steps of:

a) inducing mutagenesis in cells of a starting variety of a *Brassicaceae* or *Helianthus* species;

b) obtaining one or more progeny plants from said cells;

c) identifying at least one of said progeny plants that contains a delta-15 fatty acid desaturase gene having at least one mutation, said at least one mutation in a region encoding a His-Xaa-Xaa-Xaa-His amino acid motif; and

d) producing said plant line from said at least one progeny plant by self- or cross-pollination, said plant line having said delta-15 gene mutation.

32. A canola seed designated Q4275 and represented by ATCC accession number 97569.

33. Progeny of the seed of claim 32, said progeny having a mutant delta-12 fatty acid desaturase present in seed represented by ATCC accession number 97569.

34. The progeny of claim 33, wherein said progeny are *Brassica napus* plants.

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